

We claim:

1. A method of modulating insulin activity in mammalian cells, said method comprising administering to said cells an amino acid sequence which binds IR and comprises the amino acid sequence $X_1X_2X_3X_4X_5$, wherein X_1 , X_2 ,
5 X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid.
2. The method according to claim 1 wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
- 10 3. The method according to claim 2 wherein said amino acid sequence is an insulin agonist.
4. The method according to claim 2 wherein said amino acid sequence is an insulin antagonist.
5. The method according to claim either one of claims 3 or 4 wherein X_1 and
15 X_5 are phenylalanine and X_2 is tyrosine.
6. The method according to claim 5 wherein X_4 is tryptophan.
7. The method according to claim 6 wherein the amino acid sequence is an insulin agonist and X_3 is selected from the group consisting of aspartic acid and glutamic acid.
- 20 8. The method according to claim 7 wherein X_3 is aspartic acid to result in an amino acid sequence comprising FYDWF.

9. The method according to claim 7 wherein X₃ is glutamic acid to result in an amino acid sequence comprising FYEWF.
10. The method according to claim 1 wherein the amino acid sequence FHEN is bound to the amino terminal of X₁X₂X₃X₄X₅ to produce an amino acid sequence comprising FHENX₁X₂X₃X₄X₅ and possessing insulin agonist activity.
11. The method according to claim 10 wherein the amino acid sequence is FHENFYDWF.
12. The method according to claim 1 wherein the amino acid sequence X₁X₂X₃X₄X₅ further comprises the amino acid sequence X₉₃ X₉₄ X₉₅ X₉₆ X₉₇ located at the carboxy terminal end adjacent to X₅, wherein X₉₃, X₉₄ and X₉₇ may be any amino acid, X₉₅ is selected from the group consisting of glutamine, glutamic acid, alanine and lysine, and X₉₆ is a hydrophobic or aliphatic amino acid.
13. The method according to claim 12 wherein X₉₃ is selected from the group consisting of alanine, aspartic acid, glutamic acid, arginine, and valine, X₉₅ is glutamine or glutamic acid, and X₉₆ is selected from the group consisting of leucine, isoleucine, valine and tryptophan.
14. The method according to claim 13 wherein X₉₆ is leucine or tryptophan.
15. The method according to claim 14 wherein X₉₆ is leucine.
16. The method according to claim 13 wherein X₉₅ is glutamine or glutamic acid, and X₉₆ is tryptophan.

17. The method according to claim 13 wherein X_{95} is glutamic acid and the amino acid sequence is an insulin agonist.
18. The method according to claim 13 wherein asparagine is present as the amino acid bound to the amino terminal of X_1 and wherein $X_1X_2X_3X_4X_5X_{93}$ is FYDWFV
19. The method according to claim 1 wherein the amino acid sequence is selected from the group of amino acid sequences listed in Figures 1, 2, and 9.
20. The method according to claim 1 wherein the sequence is selected from the group consisting of FHENFYDWFVRQVSK, DYKDVTFITSAVFHENFYDWFVRQVSKK, GRVDWLQRNANFYDWFVAELG and APTFYAWFNQQT.
21. The method according to claim 1 wherein the sequence is selected from the group consisting of
- FHENFYDWFVRQVAKK-NH₂
FHENFYDWFVRQASKK-NH₂
FHENFYDWFVRAVSKK-NH₂
FHENFYDWFVAQVSKK-NH₂
FHENFYDWFARQVSKK-NH₂
FHEAFYDWFVRQVSKK-NH₂
FHANFYDWFVRQVSKK-NH₂
FAENFYDWFVRQVSKK-NH₂
AHENFYDWFVRQVSKK-NH₂
fhenfydwfvrqvskk
EFHENFYDWFVRQVSEE
FHENFYGWFVRQVSKK
HETFYSMIRSLAK
SDGFYNAIELLS
SLNFYDALQLLAKK
HDPFYSMMSLLK

NSFYEALRMLSSK
HPTSKEIYAKLLK
HPSTNQMLMKLFFK
HPPLSELKLFLIKK
5 HAPLSVLVQALLKK
HPSLSDMRWILLK
WSDFYSYFQGLD
D117-Dap(D117)
SSNFYQALMLLS
10 D117-Dap(CO-CH₂-O-NH₂)
HENFYGWFVRQVSKK
D117-Lys(D117)
D117-b-Ala-Lys(D117)
D117-b-Ala-Dap(b-Ala-D117)
15 D117-Gly-Lys(Gly-D117)
D117-b-Ala-Lys(b-Ala-D117)
D117-Dab(D117)
D117-Orn(D117)
D117-Dap(b-Ala-D117)
20 D117-b-Ala-Orn(b-Ala-D117)
1-(Thia-b-Ala-D117)₂
FHENFYDWFVRQVS
FHENFYDWFVRQVSK
FHENFYDWFVQVSK
25 FHENFYDWFVVSK
FHENFYDWFVSK
FHENFYDWFVK
FYDWF-NH₂
FYDWFKK-NH₂
30 AFYDWFakk-NH₂
AAAAFYDWFAAAAAKK-NH₂
(D117)₂-12
(Cys-Gly-D117)₂
Cys-Gly-D117
35 (D117)₂-14
LDALDRLMRYFEERPSL-NH₂
PLAELWAYFEHSEQGRSSAH-NH₂
GRVDWLQRNANFYDWFVAELG-NH₂
NGVERAGTGDNFYDWFVAQLH-NH₂
40 EHWNTVDPFYFTLFEWLRESG-NH₂
EHWNTVDPFYQYFSELLRESG-NH₂
QSDSGTVHDRFYGWFRDTWAS-NH₂
AFYDWFak-NH₂

AFYDWFA-NH₂
AFYDWF-NH₂
FYDWDA-NH₂
Ac-FYDWF-NH₂
5 Lig-FHENFYDWFVRQVSKK
Lig-GGGFHENFYDWFVRQVSKK
FHENFYDWFVRQVSKKGGG-Lig
Lig-CAWPTYWNCG
ACAWPTYWNCG-Lig
10 ACAWPTYWNCGGGG-Lig
Lig-SDGFYNAIELLS
SDGFYNAIELLS-Lig
SDGFYNAIELLSGGG-Lig
KHLCVLEELFWGASLFGYCSGKK-Lig
15 AFYDWF~~AKK~~-Lig
AFYEW~~FAKK~~-NH₂
AFYGW~~FAKK~~-NH₂
AFYKW~~FAKK~~-NH₂
(SDGFYNAIELLS-Lig)₂-14
20 (AFYDWF~~AKK~~-Lig)₂-14
FHENAYDWFVRQVSKK
FHENFADWFVRQVSKK
FHENFYAWFVRQVSKK
FHENFYDAFVRQVSKK
25 FHENFTDWA VRQVSKK
FQSLLEELVWGAPLFRYGTG
PLCVLEELFWGASLFGQCSG
QLEEEWAGVQCEVYGRECP
Cys-(Gly)₂-D117
30 (Cys-(Gly)₂-D117)₂
(S210)-14-(S212)
(S131)-14-(S212)
(S205)₂-14
(S204)₂-14
35 (S131)-14-(S210)
RVDWLQRNANFYDWFVAELG
VDWLQRNANFYDWFVAELG
DWLQRNANFYDWFVAELG
WLQRNANFYDWFVAELG
40 LQRNANFYDWFVAELG
QRNANFYDWFVAELG
RNANFYDWFVAELG
NANFYDWFVAELG

ANFYDWFVAELG
 NFYDWFVAELG
 GRVDWLQRNANFYDWFVAELG-Lig
 Lig-GRVDWLQRNANFYDWFVAELG
 5 (S208)-14-(S131)
 (S208)-14-(S209)
 GRVDWLQRNANFYDWFVAEL
 GRVDWLQRNANFYDWFVAE
 GRVDWLQRNANFYDWFVA
 10 GRVDWLQRNANFYDWFV
14-(SDGFYNAIELLS-Lig)₂
 (GRVDWLQRNANFYDWFVAELG)-14
14-(GRVDWLQRNANFYDWFVAE LG)
 (SDGFYNAIELLSGGG)₂-14
 15 H-Acy-CLEE-w-GASL-Tic-QCSG-NH₂
 RWPNFYGYFESLLTHFS-NH₂
 HYNFYEYFQVLLAETW-NH₂
 EGWDFYSYFSGLLASVT-NH₂
 LDRQFYRYFQDLLVGFM-NH₂
 20 WGRSFYRYFETLLAQGI-NH₂
 PLCFLQELFGGASLGGYCSG-NH₂
 WLEQERAWIWCEIQGSGCRA-NH₂
 IQGWEPFYGWFDVVAQMFEENH₂
 TGHRLGLDEQFYWWFRDALSG-NH₂
 25 H-Abu-CLEE-w-GASL-Tic-QCSG-NH₂
14-(Dap-CAWPTYWNCG)₂
 RDHypFYDWFDDi-NH₂
 S131-14-S209
 S294-14-S210
 30 S295-14-S210
 S294-14-204
 S295-14-S204
 GFREGQRWYWFVAQVT-NH₂
 VASGHVLHGQFYRWFVDQFALEE-NH₂
 35 VGDFCVSHDCFYGWFLRESMQ-NH₂
 DLRVLCELFGGAYVLGYCSE-NH₂
 HLSVGEELSWVALLGQWAR-NH₂
 APVSTEELRWGALLFGQWAG-NH₂
 ALEEWAQVQVRSIRSGPL-NH₂
 40 WLEHEWAQIQCELYGRGCTY-NH₂
 AAVHEQFYDWFADQYEE-NH₂
 QAPSNFYDWFVREWDEE-NH₂
 QSFYDYIEELLGGEWKK-NH₂

- DPFYQGLWEWLRESGEE-NH₂
 (S204)₂-7
 (S204)₂-9
 (S204)₂-12
 5 (S204)₂-13
 DWLQRNANFYDWFVAEL-Lig
 Lig-DWLQRNANFYDWFVAEL
 (S209)₂-9
 (S210)₂-9
 10 LigKHL CVLEELFWGASLFGYCSGKKKK
 KHL CVLEELFWGASLFGYCSGKKKK-Lig
 (S294)₂-14
 (S295)₂-14
 S-D-G-F-Y-N-A-Acy-E-L-L-S
 15 S-G-P-F-Y-E-E-Acy-E-L-L-W-Aib
 G-G-S-F-Y-D-D-Acy-E-Aib-L-W-Aib
 N-Aib-P-F-Y-D-E-Acy-D-E-Cha-W-Aib
 GRVDWLQRNANFYDWFVAEAcyG-NH₂
 and wherein underlined numbers represent a linker as defined in Table 18.
- 20 22. The method according to claim 2 wherein the amino acid sequence binds to
 the insulin receptor with an affinity of at least about 10⁻⁵ M.
23. The method according to claim 22 wherein the affinity is at least about 10⁻⁷
 M.
24. The method according to claim 23 wherein the affinity is at least about 10⁻⁹
 25 M.
25. An amino acid sequence comprising X₁X₂X₃X₄X₅ wherein X₁, X₂, X₄, and
 X₅ are aromatic amino acids, X₃ is any polar amino acid, and wherein said
 amino acid sequence binds to IGF-1R.
26. The amino acid sequence according to claim 25 wherein the IGF-1R binding
 30 occurs with an affinity (K_d) of at least about 10⁻⁵ M.

27. The amino acid sequence according to claim 25 wherein the binding occurs at an affinity (K_d) of at least about 10^{-7} M.
28. The amino acid sequence according to claim 25 wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
29. The amino acid sequence according to claim 28 wherein X_3 is selected from the group consisting of aspartic acid and glutamic acid.
30. The amino acid sequence according to claim 29 wherein X_1 and X_5 are phenylalanine and X_2 is tyrosine.
31. The amino acid sequence according to claim 29 wherein X_4 is tryptophan.
32. The amino acid sequence according to claim 31 wherein X_3 is aspartic acid to result in an amino acid sequence comprising FYDWF.
33. The amino acid sequence according to claim 31 wherein X_3 is glutamic acid to result in an amino acid sequence comprising FYEWF.
34. The amino acid sequence according to claim 28 wherein the amino acid sequence FHEN is bound to the amino terminal of $X_1X_2X_3X_4X_5$ to produce an amino acid sequence comprising FHEN $X_1X_2X_3X_4X_5$.
35. The amino acid sequence according to claim 34 wherein the amino acid sequence comprises FHENFYDWF.

36. The amino acid sequence according to claim 25 wherein the amino acid sequence $X_1X_2X_3X_4X_5$ further comprises the amino acid sequence $X_{93} X_{94} X_{95} X_{96} X_{97}$ located at the carboxy terminal end adjacent to X_5 to form $X_1X_2X_3X_4X_5X_{93}X_{94}X_{95}X_{96}X_{97}$, wherein X_{93} , X_{94} and X_{97} may be any amino acid, X_{95} is selected from the group consisting of glutamine, glutamic acid, alanine and lysine, and X_{96} is a hydrophobic or aliphatic amino acid.
37. The amino acid sequence according to claim 36 wherein X_{93} is selected from the group consisting of alanine, aspartic acid, glutamic acid, arginine, and valine, X_{95} is glutamine or glutamic acid, and X_{96} is selected from the group consisting of leucine, isoleucine, valine and tryptophan.
38. The amino acid sequence according to claim 37 wherein X_{96} is leucine or tryptophan.
39. The amino acid sequence according to claim 38 wherein X_{96} is leucine.
40. The amino acid sequence according to claim 39 wherein X_{95} is glutamine, and X_{96} is tryptophan.
41. The amino acid sequence according to claim 40 wherein X_{93} is valine.
42. The amino acid sequence according to claim 41 wherein asparagine is bound to the amino terminal of X_1 .
43. An amino acid sequence selected from the amino acid sequences listed in Figures 1-A through 1-O.

44. The amino acid sequence according to claim 25 wherein the sequence is selected from the group consisting of FHENFYDWFVRQVS, DYKDVTFTSAVFHENFYDWFVRQVSKK, GRVDWLQRNANFYDWFVAELG and APTFYAWFNQQT.

5 45. The amino acid sequence according to claim 25 wherein the sequence comprises FHENFYDWFVRQVS.

46. The amino acid sequence according to claim 25 wherein the sequence is selected from the group consisting of

10 FHENFYDWFVRQVAKK-NH₂
FHENFYDWFVRQASKK-NH₂
FHENFYDWFVRAVSKK-NH₂
FHENFYDWFVAQVSKK-NH₂
FHENFYDWFARQVSKK-NH₂
FHEAFYDWFVRQVSKK-NH₂
15 FHANFYDWFVRQVSKK-NH₂
FAENFYDWFVRQVSKK-NH₂
AHENFYDWFVRQVSKK-NH₂
fhenfydwfvrqvskk
EFHENFYDWFVRQVSEE
20 FHENFYGWFVRQVSKK
HETFYSMIRSLAK
SDGFYNAIELLS
SLNFYDALQLLAKK
HDPFYSMMSLLK
25 NSFYEALRMLSSK
HPTSKEIYAKLLK
HPSTNQMLMKLKF
HPPLSELKLFLIKK
HAPLSVLVQALLKK
30 HPSLSDMRWILLK
WSDFYSYFQGLD
D117-Dap(D117)
SSNFYQALMLLS
D117-Dap(CO-CH₂-O-NH₂)
35 HENFYGWFVRQVSKK
D117-Lys(D117)

D117-b-Ala-Lys(D117)
D117-b-Ala-Dap(b-Ala-D117)
D117-Gly-Lys(Gly-D117)
D117-b-Ala-Lys(b-Ala-D117)
5 D117-Dab(D117)
D117-Orm(D117)
D117-Dap(b-Ala-D117)
D117-b-Ala-Orm(b-Ala-D117)
1-(Thia-b-Ala-D117)₂
10 FHENFYDWFVRQVS
FHENFYDWFVRQVSK
FHENFYDWFVQVSK
FHENFYDWFVVSK
FHENFYDWFVSK
15 FHENFYDWFVK
FYDWF-NH₂
FYDWFKK-NH₂
AFYDWFakk-NH₂
AAAAFYDWFAAAAKK-NH₂
20 (D117)₂-12
(Cys-Gly-D117)₂
Cys-Gly-D117
(D117)₂-14
LDALDRLMRYFEERPSL-NH₂
25 PLAELWAYFEHSEQGRSSAH-NH₂
GRVDWLQRNANFYDWFVAELG-NH₂
NGVERAGTGDNFYDWFVAQLH-NH₂
EHWNTVDPFYFTLFEWLRESG-NH₂
EHWNTVDPFYQYFSELLRESG-NH₂
30 QSDSGTVHDRFYGWFRDTWAS-NH₂
AFYDWFak-NH₂
AFYDWFa-NH₂
AFYDWF-NH₂
FYDWDA-NH₂
35 Ac-FYDWF-NH₂
Lig-FHENFYDWFVRQVSKK
Lig-GGGFHENFYDWFVRQVSKK
FHENFYDWFVRQVSKKGGG-Lig
Lig-CAWPTYWNCG
40 ACAWPTYWNCG-Lig
ACAWPTYWNCGGGG-Lig
Lig-SDGFYNAIELLS
SDGFYNAIELLS-Lig

SDGFYNAIELLSGGG-Lig
 KHLCVLEELFWGASLFGYCSGKK-Lig
 AFYDWFACK-Lig
 AFYEWFAKK-NH₂
 5 AFYGWFAKK-NH₂
 AFYKWFAKK-NH₂
 (SDGFYNAIELLS-Lig)₂-14
 (AFYDWFACK-Lig)₂-14
 FHENAYDWFVRQVSCK
 10 FHENFADWFVRQVSCK
 FHENFYAWFVRQVSCK
 FHENFYDAFVRQVSCK
 FHENFTDWAVRQVSCK
 FQSLLEELVWGAPLFRYGTG
 15 PLCVLEELFWGASLFGQCSG
 QLEEEWAGVQCEVYGRECPS
 Cys-(Gly)₂-D117
 (Cys-(Gly)₂-D117)₂
 (S210)-14-(S212)
 20 (S131)-14-(S212)
 (S205)₂-14
 (S204)₂-14
 (S131)-14-(S210)
 RVDWLQRNANFYDWFVAELG
 25 VDWLQRNANFYDWFVAELG
 DWLQRNANFYDWFVAELG
 WLQRNANFYDWFVAELG
 LQRNANFYDWFVAELG
 QRNANFYDWFVAELG
 30 RNANFYDWFVAELG
 NANFYDWFVAELG
 ANFYDWFVAELG
 NFYDWFVAELG
 GRVDWLQRNANFYDWFVAELG-Lig
 35 Lig-GRVDWLQRNANFYDWFVAELG
 (S208)-14-(S131)
 (S208)-14-(S209)
 GRVDWLQRNANFYDWFVAEL
 GRVDWLQRNANFYDWFVAE
 40 GRVDWLQRNANFYDWFVA
 GRVDWLQRNANFYDWFV
14-(SDGFYNAIELLS-Lig)₂
 (GRVDWLQRNANFYDWFVAELG)-14

14-(GRVDWLQRNANFYDWFVAE LG)
 (SDGFYNAIELLSGGG)₂-14
 H-Acy-CLEE-w-GASL-Tic-QCSG-NH₂
 RWPNFYGYFESLLTHFS-NH₂
 5 HYNIFYEYFQVLLAETW-NH₂
 EGWDFYSYFSGLLASVT-NH₂
 LDRQFYRYFQDLLVGFM-NH₂
 WGRSFYRYFETLLAQGI-NH₂
 PLCFLQELFGGASLGGYCSG-NH₂
 10 WLEQERAWIWCEIQSGGCRA-NH₂
 IQGWEPFYGWFDVVVAQMFEENH₂
 TGHRLGLDEQFYWWFRDALSG-NH₂
 H-Abu-CLEE-w-GASL-Tic-QCSG-NH₂
14-(Dap-CAWPTYWNCG)₂
 15 RDHypFYDWFDDi-NH₂
 S131-14-S209
 S294-14-S210
 S295-14-S210
 S294-14-204
 20 S295-14-S204
 GFREGQRWYWFVAQVT-NH₂
 VASGHVLHGQFYRWFVDQFALEE-NH₂
 VGDFCVSHDCFYGWFLRESMQ-NH₂
 DLRVLCELFGGAYVLGYCSE-NH₂
 25 HLSVGEELSWVALLGQWAR-NH₂
 APVSTEELRWGALLFGQWAG-NH₂
 ALEEEWAWVQVRSIRSGPL-NH₂
 WLEHEWAQIQCELYGRGCTY-NH₂
 AAVHEQFYDWFADQYEE-NH₂
 30 QAPSNFYDWFVREWDEE-NH₂
 QSFYDYIEELLGGEWKK-NH₂
 DPFYQGLWEWLRESGEE-NH₂
 (S204)₂-7
 (S204)₂-9
 35 (S204)₂-12
 (S204)₂-13
 DWLQRNANFYDWFVAEL-Lig
 Lig-DWLQRNANFYDWFVAEL
 (S209)₂-9
 40 (S210)₂-9
 LigKHLCVLEELFWGASLFGYCSGKKKK
 KHLCVLEELFWGASLFGYCSGKKKK-Lig
 (S294)₂-14

(S295)₂-14

S-D-G-F-Y-N-A-Acy-E-L-L-S

S-G-P-F-Y-E-E-Acy-E-L-L-W-Aib

G-G-S-F-Y-D-D-Acy-E-Aib-L-W-Aib

5 N-Aib-P-F-Y-D-E-Acy-D-E-Cha-W-Aib

GRVDWLQRNANFYDWFVAEAcyG-NH₂

and wherein underlined numbers represent a linker as defined in Table 18.

47. An amino acid sequence which specifically binds IR such that binding to IGF-1R is at or below background and wherein said amino acid sequence
10 comprises X₁X₂X₃X₄X₅ wherein X₁, X₂, and X₅ are selected from the group consisting of phenylalanine and tyrosine, X₃ is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X₄ is selected from group consisting of tryptophan, tyrosine and phenylalanine.
48. A method of modulating insulin activity in mammalian cells, said method
15 comprising administering to said cells an amino acid sequence which binds IR and comprises the sequence of amino acids X₆X₇X₈X₉X₁₀X₁₁X₁₂X₁₃ wherein X₆ and X₇ are aromatic amino acids or glutamine, X₈, X₉, X₁₁ and X₁₂ may be any amino acid, X₁₀ and X₁₃ are hydrophobic amino acids.
49. The method according to claim 48 wherein X₆ and X₇ are selected from
20 group consisting of phenylalanine and tyrosine, and X₁₀ and X₁₃ are selected from group consisting of leucine, isoleucine, tryptophan, phenylalanine methionine and valine.
50. The method according to claim 48 wherein X₆ is phenylalanine and X₇ is tyrosine.
- 25 51. The method according to claim 50 wherein X₁₀ is isoleucine.
52. The method according to claim 50 wherein X₁₀ is leucine.

53. The method according to claim 50 wherein X_{13} is leucine.
54. The method according to claim 50 wherein X_9 is tyrosine and X_{10} is phenylalanine.
55. The method according to claim 50 wherein the amino acid sequence is
5 selected from $FYX_8X_9LX_{11}X_{12}L$, $FYX_8X_9IX_{11}X_{12}L$ and $FYX_8YFX_{11}X_{12}L$.
56. The method according to claim 55 wherein the amino acid sequence comprises $FYX_8X_9LX_{11}X_{12}L$.
57. The method according to claim 55 wherein the amino acid sequence comprises $FYX_8YFX_{11}X_{12}L$.
- 10 58. The method according to claim 48 wherein the amino acid sequence $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$ further comprises amino acids X_{98} and X_{99} at the amino terminal end and X_{100} at the carboxy terminal end to form $X_{98}X_{99}X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{100}$ and wherein X_{98} is optionally aspartic acid and X_{99} is independently an amino acid selected from the group
15 consisting of glycine, glutamine and proline, and X_{100} is a hydrophobic amino acid.
59. The method according to claim 58 wherein X_{100} is an aliphatic amino acid.
60. The method according to claim 59 wherein X_{100} is leucine.
61. The method according to claim 48 wherein the amino acid sequence binds to
20 the insulin receptor with an affinity of at least about 10^{-5} M.

62. The method according to claim 61 wherein the affinity is between about 10^{-7} M.
63. The method according to claim 48 wherein the amino acid sequence comprises DYKDFYDAIDQLVRGSARAGGTRD or
5 KDRAFYNGLRDLVGAVYGAWD.
64. The method according to claim 48 wherein the amino acid sequence is selected from the group of amino acid sequences listed in Figures 2A through 2P.
65. An amino acid sequence comprising $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$ wherein X_6
10 and X_7 are aromatic amino acids or glutamine, X_8 , X_9 , X_{11} and X_{12} may be any amino acid, X_{10} and X_{13} are hydrophobic amino acids and wherein said amino acid sequence binds to IGF-1R.
66. The amino acid sequence according to claim 65 wherein the binding occurs at an affinity (K_d) of at least about 10^{-5} M.
- 15 67. The amino acid sequence according to claim 66 wherein the binding occurs at an affinity (K_d) of at least about 10^{-7} M.
68. The amino acid sequence according to claim 65 wherein X_6 and X_7 are phenylalanine or tyrosine, and X_{10} and X_{13} are leucine, isoleucine, tryptophan, phenylalanine or methionine.
- 20 69. The amino acid sequence according to claim 68 wherein X_6 is phenylalanine and X_7 is tyrosine.

70. The amino acid sequence according to claim 68 wherein X_{10} is isoleucine.
71. The amino acid sequence according to claim 68 wherein X_{10} is leucine.
72. The amino acid sequence according to claim 69 wherein X_{13} is leucine.
- 5 73. The amino acid sequence according to claim 69 wherein X_9 is tyrosine and X_{10} is phenylalanine.
74. The amino acid sequence according to claim 68 wherein the amino acid sequence comprises an amino acid sequence selected from $FYX_8X_9LX_{11}X_{12}L$, $FYX_8X_9IX_{11}X_{12}L$ and $FYX_8YFX_{11}X_{12}L$.
- 10 75. The amino acid sequence according to claim 74 wherein the amino acid sequence comprises $FYX_8X_9IX_{11}X_{12}L$.
76. The amino acid sequence according to claim 74 wherein the amino acid sequence comprises $FYX_8X_9LX_{11}X_{12}L$.
77. The amino acid sequence according to claim 74 wherein the amino acid sequence is $FYX_8YFX_{11}X_{12}L$.
- 15 78. The amino acid sequence according to claim 65 wherein the amino acid sequence $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$ further comprises amino acids X_{98} and X_{99} at the amino terminal end and X_{100} at the carboxy terminal end to form $X_{98}X_{99}X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{100}$ and wherein X_{98} is optionally aspartic acid and X_{99} is independently an amino acid selected from the group
- 20 consisting of glycine, glutamine and proline, and X_{100} is a hydrophobic amino acid.

79. The amino acid sequence according to claim 78 wherein X_{100} is an aliphatic amino acid.
80. The amino acid sequence according to claim 79 wherein X_{100} is leucine.
- 5 81. The amino acid sequence according to claim 68 wherein the amino acid sequence comprises DYKDFYDAIDQLVRGSARAGGTRD or KDRAFYNGLRDLVGAVYGAWDKK.
82. The sequence according to claim 81 wherein the amino acid sequence comprises DYKDFYDAIDQLVRGSARAGGTRD.
- 10 83. An amino acid sequence comprising an amino acid sequence selected from the group consisting of amino sequences listed in Figures 2A through 2P.
84. An amino acid sequence comprising a sequence selected from the group consisting of
- 15 SFYEAHQLLGV,
NSFYALRMLSS,
SLNFYDALQLLA,
SSNFYQALMLLS,
SDGFYNAIELLS,
HETFYSMIRSLA,
20 HDPFYSMMKSL and
WSDFYSYFQGLD.

85. The amino acid sequence according to claim 65 wherein the sequence comprises the amino acid sequence
X₁₁₅X₁₁₆X₁₁₇X₁₁₈FYX₈YFX₁₁X₁₂LX₁₁₉X₁₂₀X₁₂₁X₁₂₂ wherein X₁₁₅ is selected from the group consisting of tryptophan, glycine, aspartic acid, glutamic acid and arginine, X₁₁₆ is selected from the group consisting of aspartic acid, histidine, glycine and asparagine, X₁₁₇ and X₁₁₈ are selected from the group consisting of glycine, aspartic acid, glutamic acid, asparagine, and alanine, X₈ is selected from the group consisting of arginine, glycine, glutamic acid and serine, X₁₁ is selected from the group consisting of glutamic acid, asparagine, glutamine and tryptophan, X₁₂ is selected from the group consisting of aspartic acid, glutamic acid, glycine, lysine, and glutamine, X₁₁₉ is selected from the group consisting of glutamic acid, glycine, glutamine, aspartic acid and alanine, X₁₂₀ is selected from the group consisting of glutamic acid, aspartic acid, glycine and glutamine, X₁₂₁ is selected from the group consisting of tryptophan, tyrosine, glutamic acid, phenylalanine, histidine and aspartic acid, and X₁₂₂ is selected from the group consisting of glutamic acid, aspartic acid, and glycine.
86. The amino acid sequence according to claim 85 wherein X₁₁₅ is tryptophan, X₁₁₇ is selected from glycine, aspartic acid, glutamic acid and asparagine; X₁₁₈ is selected from glycine, aspartic acid, glutamic acid and alanine; X₁₁, X₁₁₉, X₁₂₀, and X₁₂₂ are glutamic acid; X₁₂ is aspartic acid, and X₁₂₁ is tryptophan or tyrosine.
87. An amino acid sequence comprising X₆X₇X₈X₉X₁₀X₁₁X₁₂X₁₃ wherein X₆ and X₇ are aromatic amino acids or glutamine, X₈, X₉, X₁₁ and X₁₂ may be any amino acid, X₁₀ and X₁₃ are hydrophobic amino acids and wherein said amino acid sequence binds to IR such that binding to IGF-1R is at or below background.

88. A method of binding to Site 1 of IR from mammalian cells, said method comprising contacting IR with an amino acid sequence which binds IR and comprises the sequence of $X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}$ wherein X_{14} , X_{17} , and X_{18} are hydrophobic amino acids, X_{15} , X_{16} , and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids.
89. The method according to claim 88 wherein X_{14} and X_{17} are selected from the group consisting of leucine, isoleucine and valine; X_{20} is selected from group consisting of tyrosine and histidine; and X_{21} is selected from group consisting of phenylalanine and tyrosine.
90. The method according to claim 89 wherein X_{14} and X_{17} are leucine.
91. The method according to claim 89 wherein X_{14} is leucine.
92. The method according to claim 89 wherein X_{17} is leucine.
93. The method according to claim 89 wherein X_{20} is tyrosine.
94. The method according to claim 89 wherein X_{21} is phenylalanine.
95. The method according to claim 90 wherein X_{15} is a large amino acid.
96. The method according to claim 89 wherein said amino acid sequence further comprises an amino acid extension comprising $X_{101}X_{102}X_{103}$ wherein X_{103} is bound to X_{14} at the amino terminus and X_{101} and X_{102} are polar amino acids and X_{103} is a hydrophobic amino acid.
97. The method according to claim 96 wherein X_{101} and X_{102} are independently aspartic acid or glutamic acid and X_{103} is leucine, isoleucine or valine.

98. A method of binding to Site 1 of IGF-1R from mammalian cells, said method comprising contacting IGF-1R with an amino acid sequence which binds IR and comprises the sequence of $X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}$ wherein X_{14} , X_{17} , and X_{18} are hydrophobic amino acids, X_{15} , X_{16} , and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids.
99. The method according to claim 98 wherein X_{14} and X_{17} are selected from the group consisting of leucine, isoleucine and valine; X_{18} is an aromatic amino acid; X_{20} is selected from group consisting of tyrosine and histidine; and X_{21} is selected from group consisting of phenylalanine and tyrosine.
100. The method according to claim 98 wherein the amino acid sequence comprises a sequence selected from the sequences in Figures 3A through 3D.
101. An amino acid sequence which binds Site 1 of IR from mammalian cells, said sequence comprising $X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}$ wherein X_{14} , X_{17} , and X_{18} are hydrophobic amino acids, X_{15} , X_{16} , and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids.
102. The amino acid sequence according to claim 101 wherein X_{14} and X_{17} are selected from the group consisting of leucine, isoleucine and valine; X_{20} is selected from group consisting of phenylalanine and tyrosine.
103. The amino acid sequence according to claim 102 wherein X_{14} and X_{17} are leucine.
104. The amino acid sequence according to claim 102 wherein X_{14} is leucine.
105. The amino acid sequence according to claim 102 wherein X_{17} is leucine.

106. The amino acid sequence according to claim 102 wherein amino acid X_{18} is tryptophan.
107. The amino acid sequence according to claim 103 wherein X_{20} is tyrosine.
108. The amino acid sequence according to claim 107 wherein X_{21} is
5 phenylalanine.
109. The amino acid sequence according to claim 103 wherein X_{15} is a large amino acid.
110. The amino acid sequence according to claim 101 wherein at least one amino acid is a D-amino acid.
- 10 111. The amino acid sequence according to claim 65 wherein at least one amino acid is a D-amino acid.
112. The amino acid sequence according to claim 102 wherein said amino acid sequence further comprises an amino acid extension comprising
15 $X_{101}X_{102}X_{103}$ wherein X_{103} is bound to X_{14} at the amino terminus and X_{101} and X_{102} are polar amino acids and X_{103} is a hydrophobic amino acid.
113. The amino acid sequence according to claim 112 wherein X_{101} and X_{102} are independently aspartic acid or glutamic acid and X_{103} is leucine, isoleucine or valine.

114. An amino acid sequence which binds Site 1 of IGF-1R from mammalian cells such that binding to IR is at or below background, said sequence comprising $X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}$ wherein X_{14} , X_{17} , and X_{18} are hydrophobic amino acids, X_{15} , X_{16} , and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids.
115. The amino acid sequence according to claim 114 wherein X_{14} and X_{17} are selected from the group consisting of leucine, isoleucine and valine; X_{18} is an aromatic amino acid; X_{20} is selected from group consisting of tyrosine and histidine; and X_{21} is selected from group consisting of phenylalanine and tyrosine.
116. A method of binding to Site 2 of IR from mammalian cells, said method comprising contacting said cells with an amino acid sequence comprising $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$ wherein X_{22} , X_{25} , X_{26} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{37} , X_{38} , X_{40} and X_{41} are any amino acid; X_{23} is any hydrophobic amino acid; X_{27} is a polar amino acid; X_{31} is an aromatic amino acid; X_{32} is a small amino acid; and wherein at least one cysteine is located at positions X_{24} through X_{27} and one at X_{39} or X_{40} .
117. The method according to claim 116 wherein X_{24} and X_{39} are cysteines.
118. The method according to claim 117 wherein X_{23} is selected from leucine, isoleucine, methionine and valine; X_{27} is selected from glutamic acid, aspartic acid, asparagine, and glutamine; X_{31} is tryptophan, X_{32} is glycine; and X_{36} is any aromatic amino acid.
119. The method according to claim 118 wherein the binding to IR occurs at an affinity (K_d) of at least about 10^{-5} M.

120. The method according to claim 116 wherein X_{23} is leucine, X_{27} is glutamic acid, X_{31} is tryptophan, and X_{32} is glycine.
121. The method according to claim 116 wherein the amino acid sequence is HLCVLEELFWGASLFGYCSG.
- 5 122. An amino acid sequence which binds IR, said amino acid sequence comprising
 $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$
wherein X_{22} , X_{25} , X_{26} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{37} , X_{38} , X_{40} and X_{41} are
any amino acid, X_{23} is any hydrophobic amino acid, X_{27} is a polar amino
10 acid; X_{31} is an aromatic amino acid; X_{32} is a small amino acid, and wherein
at least one cysteine is located at positions X_{24} through X_{27} and one at X_{39} or
 X_{40} .
123. The amino acid sequence according to claim 122 wherein X_{24} and X_{39} are
cysteines.
- 15 124. The amino acid sequence according to claim 123 wherein X_{23} is selected
from methionine, valine, and leucine; X_{27} is selected from glutamic acid,
alanine, glycine, glutamine, aspartic acid and valine; X_{31} and X_{32} are small
amino acids; and X_{36} is an aromatic amino acid.
- 20 125. The amino acid sequence according to claim 122 wherein the binding to IR
occurs at an affinity (K_d) of at least about 10^{-5} M.
126. The amino acid sequence according to claim 124 wherein X_{23} is leucine, X_{27}
is glutamic acid, X_{31} is tryptophan, and X_{32} is glycine.

127. The amino acid sequence according to claim 122 wherein the amino acid sequence is HLCVLEELFWGASLFGYCSG.
128. A method of modulating insulin activity in mammalian cells, said method comprising administering to said cells an amino acid sequence which binds IR and comprises the sequence $X_{42} X_{43} X_{44} X_{45} X_{46} X_{47} X_{48} X_{49} X_{50} X_{51} X_{52} X_{53} X_{54} X_{55} X_{56} X_{57} X_{58} X_{59} X_{60} X_{61}$ wherein X_{42} , X_{43} , X_{44} , X_{45} , X_{53} , X_{55} , X_{56} , X_{58} , X_{60} and X_{61} are any amino acid; X_{43} , X_{46} , X_{49} , X_{50} and X_{54} are hydrophobic amino acids; X_{47} and X_{59} are cysteines; X_{48} is a polar amino acid; X_{51} , X_{52} and X_{57} are small amino acids.
129. The method according to claim 128 wherein X_{43} and X_{46} are leucine; X_{48} is selected from the group consisting of aspartic acid and glutamic acid; X_{50} is phenylalanine or tyrosine; and X_{51} , X_{52} and X_{57} are glycine.
130. The method according to claim 129 wherein X_{48} is glutamic acid and X_{50} is a phenylalanine.
131. The method according to claim 130 wherein the amino acid sequence is $X_{42} X_{43} X_{44} X_{45} LCE X_{49} FGG X_{53} X_{54} X_{55} X_{56} GX_{58} C X_{60} X_{61}$.
132. The method according the claim 131 wherein the amino acid sequence comprises DLRVLCELFGGAYVLGYCSE or DLRVLCELFGGAYVRGYCSE.
133. The method according to claim 128 wherein the binding to IR occurs at an affinity (K_d) of at least about 10^{-5} M.

134. An amino acid sequence which binds IR, said amino acid sequence comprising X_{42} X_{43} X_{44} X_{45} X_{46} X_{47} X_{48} X_{49} X_{50} X_{51} X_{52} X_{53} X_{54} X_{55} X_{56} X_{57} X_{58} X_{59} X_{60} X_{61} wherein X_{42} , X_{43} , X_{44} , X_{45} , X_{53} , X_{55} , X_{60} and X_{61} are any amino acid; X_{43} , X_{46} , X_{49} , X_{50} and X_{54} are hydrophobic amino acids; X_{47} and X_{59} are cysteines; X_{48} is a polar amino acid; and X_{51} , X_{52} and X_{57} are small amino acids.
135. The amino acid sequence according to claim 134 wherein X_{43} and X_{46} are leucine; X_{48} is selected from the group consisting of aspartic acid and glutamic acid; X_{50} is phenylalanine or tyrosine; and X_{51} , X_{52} and X_{57} are glycine.
136. The amino acid sequence according to claim 135 wherein X_{48} is glutamic acid and X_{50} is phenylalanine.
137. The amino acid sequence according to claim 136 wherein the amino acid sequence comprises X_{43} X_{44} X_{45} LCE X_{49} FGG X_{53} X_{54} X_{55} X_{56} G X_{58} C X_{60} X_{61} .
138. The amino acid sequence according to claim 137 wherein an amino acid sequence comprises DLRVLCELFGGAYVLGYCSE or DLRVLCELFGGAYVRGYCSE
139. A method of modulating insulin activity in mammalian cells, said method comprising administering to said cells an amino acid sequence comprising X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81} wherein X_{62} , X_{65} , X_{66} X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.

157. A method of modulating insulin activity in mammalian cells, said method comprising administering to said cells an amino acid sequence which binds IR and comprises $HX_{82}X_{83}X_{84}X_{85}X_{86}X_{87}X_{88}X_{89}X_{90}X_{91}X_{92}$ herein X_{82} is proline or alanine; X_{83} is a small amino acid; X_{84} is selected from the group consisting of leucine, serine and threonine; X_{85} is a polar amino acid; X_{86} is any amino acid; X_{87} is an aliphatic amino acid; X_{88} , X_{89} , X_{90} is any amino acid; and X_{91} and X_{92} are aliphatic amino acids.
158. The method according to claim 157 wherein X_{82} is proline; X_{83} is selected from the group consisting of proline, serine and threonine; X_{84} is leucine; X_{85} is selected from the group consisting of glutamic acid, serine, lysine and asparagine; X_{86} is a polar amino acid; X_{87} is selected from the group consisting of leucine, methionine and isoleucine; and X_{91} and X_{92} are leucines.
159. The method according to claim 158 wherein X_{83} is proline.
160. The method according to claim 158 wherein X_{85} is serine.
161. The method according to claim 158 wherein X_{86} is selected from the group consisting of histidine, glutamic acid, aspartic acid and glutamine.
162. The method according to claim 158 wherein X_{87} is leucine.
163. The method according to claim 158 wherein X_{92} is phenylalanine.
164. The method according to claim 160 wherein the amino acid sequence is $HPPLSX_{86}LX_{88}X_{89}X_{90}LL$.

165. The method according to claim 158 wherein the amino acid sequence is selected from the group consisting of HPPLEHLKAFLI, HPPLSELKLFLI, HPSLSDMRWILL, HPTSKEIYAKLL, HPTSKEIYAKLL, HPSTNQMLMKLF and HAPLSVLQALL.
- 5 166. An amino acid sequence which binds IR, said amino acid sequence comprising $HX_{82}X_{83}X_{84}X_{85}X_{86}X_{87}X_{88}X_{89}X_{90}X_{91}X_{92}$ herein X_{82} is proline or alanine; X_{83} is a small amino acid; X_{84} is selected from the group consisting of leucine, serine and threonine; X_{85} is a polar amino acid; X_{86} is any amino acid; X_{87} is an aliphatic amino acid; X_{88} , X_{89} , X_{90} is any amino acid; and X_{91} and X_{92} are aliphatic amino acids.
- 10
167. The amino acid sequence according to claim 166 wherein X_{82} is proline; X_{83} is selected from the group consisting of proline, serine and threonine; X_{84} is leucine; X_{85} is selected from the group consisting of glutamic acid, serine, lysine and asparagine; X_{86} is a polar amino acid; X_{87} is selected from the group consisting of leucine, methionine and isoleucine; and X_{91} and X_{92} are leucines.
- 15
168. The amino acid sequence according to claim 167 wherein X_{83} is proline.
169. The amino acid sequence according to claim 167 wherein X_{85} is serine.
170. The amino acid sequence according to claim 167 wherein X_{86} is selected from the group consisting of histidine, glutamic acid, aspartic acid and glutamine.
- 20
171. The amino acid sequence according to claim 167 wherein X_{87} is leucine.

172. The amino acid sequence according to claim 167 wherein X₉₂ is phenylalanine.
173. The amino acid sequence according to claim 169 wherein the amino acid sequence is HPPLSX₈₆ LX₈₈ X₈₉ X₉₀ LL.
- 5 174. The amino acid sequence according to claim 167 wherein the amino acid sequence is selected from the group consisting of HPPLEHLKAFLI, HPPLSELKLFLI, HPSLSDMRWILL, HPTSKEIYAKLL, HPTSKEIYAKLL, HPSTNQMLMKLF and HAPLSVLQALL.
- 10 175. A method modulating insulin activity in mammalian cells, said method comprising administering to said cells an amino acid sequence comprising an amino acid sequence of X₁₀₄X₁₀₅X₁₀₆X₁₀₇X₁₀₈X₁₀₉X₁₁₀X₁₁₁X₁₁₂X₁₁₃X₁₁₄ wherein at least one of the amino acids of X₁₀₆ through X₁₁₁ are tryptophan; wherein X₁₀₄ and X₁₁₄ are both small amino acids; wherein X₁₀₅ is any amino acid; and wherein at least one of X₁₀₄, X₁₀₅, X₁₀₆ and one of X₁₁₂ X₁₁₃ X₁₁₄ are cysteine residues.
- 15
176. The method according to claim 175 wherein at least two of the amino acids of X₁₀₆ through X₁₁₁ are tryptophan which are separated from each other by at least two amino acids.
177. The method according to claim 176 wherein the separating amino acids are selected from the group consisting of proline, threonine and tyrosine.
- 20
178. The method according to claim 177 wherein the amino acid sequence comprises WPTYW.

179. The method according to claim 178 wherein X_{105} and X_{113} are cysteine residues.
180. The method according to claim 178 wherein X_{104} and X_{114} are selected from the group consisting of alanine and glycine.
- 5 181. The method according to claim 180 wherein X_{104} is alanine and X_{114} is glycine.
182. The method according to claim 181 wherein X_{105} is valine.
183. The method according to claim 182 wherein X_{112} is asparagine.
184. The method according to claim 198 wherein the affinity (K_d) of binding to
10 IR is at least about 10^{-5} M.
185. A method of modulating insulin activity in mammalian cells, said method comprising administering to said cells an amino acid sequence comprising an amino acid sequence selected from the group listed in Figure 8.
186. The method according to claim 185 wherein the sequence comprises
15 ACVWPTYWNCG.
187. An amino acid sequence which binds and IR and comprising an amino acid sequence of $X_{104}X_{105}X_{106}X_{107}X_{108}X_{109}X_{110}X_{111}X_{112}X_{113}X_{114}$ wherein at least one of the amino acids of X_{106} through X_{111} are tryptophan; wherein X_{104} and X_{114} are both small amino acids; wherein X_{105} is any amino acid; and
20 wherein at least one of X_{104} , X_{105} , X_{106} and one of X_{112} X_{113} X_{114} are cysteine residues.

188. The amino acid sequence according to claim 187 wherein at least two of the amino acids of X₁₀₆ through X₁₁₁ are tryptophan which are separated from each other by at least two amino acids.
- 5 189. The amino acid sequence according to claim 188 wherein the separating amino acids are selected from the group consisting of proline, threonine and tyrosine.
190. The amino acid sequence according to claim 189 wherein the amino acid sequence comprises WPTYW.
- 10 191. The amino acid sequence according to claim 190 wherein X₁₀₅ and X₁₁₃ are cysteine residues.
192. The amino acid sequence according to claim 190 wherein X₁₀₄ and X₁₁₄ are selected from the group consisting of alanine and glycine.
193. The amino acid sequence according to claim 190 wherein X₁₀₄ is alanine and X₁₁₄ is glycine.
- 15 194. The amino acid sequence according to claim 193 wherein X₁₀₅ is valine.
195. The amino acid sequence according to claim 194 wherein X₁₁₂ is asparagine.
196. The amino acid sequence according to claim 202 wherein the affinity (K_d) of binding to IR is at least about 10⁻⁵ M.
- 20 197. An amino acid sequence which binds IR from mammalian cells comprising an amino acid sequence selected from the group listed in Figure 8.

198. The amino acid sequence according to claim 197 comprising
ACVWPTYWNCG.
199. A method of providing insulin agonist activity to mammalian cells, said
method comprising administering to said cells an amino acid sequence
5 comprising DYKDLQSWGVRIGWLAGLCPKK.
200. A method of modulating insulin activity in mammalian cells, said method
comprising administering to said cells an amino acid sequence comprising
an amino acid sequence selected from the group listed in Figures 9 through
11.
- 10 201. An amino acid sequence comprising DYKDLQSWGVRIGWLAGLCPKK.
202. An amino acid sequence comprising an amino acid sequence selected from
the group listed in Figures 9 through 11.
203. An amino acid sequence comprising at least two amino acid sequences
which independently bind IR, with the proviso that at least one of the
15 sequences is not insulin or a fragment thereof.
204. The amino acid sequence according to claim 203 wherein the two amino
acid sequences bind to Site 1 of IR.
205. The amino acid sequence according to claim 203 wherein one amino acid
sequence binds to Site 1, and the other binds to Site 2 of IR.

206. The amino acid sequence according to claim 203, wherein at least one of the sequences is selected from the group consisting of $X_1X_2X_3X_4X_5$ wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 may be any polar amino acid; $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$ wherein X_6 and X_7 are aromatic amino acids or glutamine, X_8 , X_9 , X_{11} and X_{12} may be any amino acid, X_{10} and X_{13} are hydrophobic amino acids; and $X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}$ wherein X_{14} , X_{17} , and X_{18} are hydrophobic amino acids, X_{15} , X_{16} , and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids.
207. The amino acid sequence according to claim 206, wherein at least one of the sequences is $X_1X_2X_3X_4X_5$ wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 may be any polar amino acid.
208. The amino acid sequence according to claim 206 wherein at least one of the sequences comprises FYX_3WF .
209. The amino acid sequence according to claim 206, wherein at least one of the sequences comprises $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$ wherein X_6 and X_7 are aromatic amino acids or glutamine, X_8 , X_9 , X_{11} and X_{12} may be any amino acid, X_{10} and X_{13} are hydrophobic amino acids.
210. The amino acid sequence according to claim 209, wherein at least one of the sequences comprises $FYX_8X_9LX_{11}X_{12}L$.
211. The amino acid sequence according to claim 206, wherein at least one of the sequences comprises $X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}$ wherein X_{14} , X_{17} , and X_{18} are hydrophobic amino acids, X_{15} , X_{16} , and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids.

212. The amino acid sequence according to claim 211 wherein at least one of the sequences comprises LX₁₅, X₁₆, LLX₁₉YF.

213. The amino acid sequence according to claim 203 wherein at least one of the sequences comprises

5 X₂₂X₂₃X₂₄X₂₅X₂₆X₂₇X₂₈X₂₉X₃₀X₃₁X₃₂X₃₃X₃₄X₃₅X₃₆X₃₇X₃₈X₃₉X₄₀X₄₁
 wherein X₂₂, X₂₅, X₂₆, X₂₈, X₂₉, X₃₀, X₃₃, X₃₄, X₃₅, X₃₆, X₃₇, X₃₈, X₄₀, and
 X₄₁ are any amino acid, X₂₃ is any hydrophobic amino acid; X₂₇ is a polar
 amino acid; X₃₁ is an aromatic amino acid; X₃₂ is a small amino acid, and
 wherein at least one cysteine is located at positions X₂₄ through X₂₇ and one
 10 at X₃₉ or X₄₀; X₄₂ X₄₃ X₄₄ X₄₅ X₄₆ X₄₇ X₄₈ X₄₉ X₅₀ X₅₁ X₅₂ X₅₃ X₅₄ X₅₅
 X₅₆X₅₇X₅₈X₅₉ X₆₀ X₆₁ wherein X₄₂, X₄₃, X₄₄, X₄₅, X₅₃, X₅₅, X₅₆, X₅₈, X₆₀ and
 X₆₁ are any amino acid; X₄₃, X₄₆, X₄₉, X₅₀ and X₅₄ are hydrophobic amino
 acids; X₄₇ and X₅₉ are cysteine; X₄₈ is a polar amino acid; and X₅₁, X₅₂ and
 X₅₇ are small amino acids; or X₆₂ X₆₃ X₆₄ X₆₅ X₆₆ X₆₇ X₆₈ X₆₉ X₇₀ X₇₁ X₇₂
 15 X₇₃ X₇₄ X₇₅ X₇₆ X₇₇ X₇₈ X₇₉ X₈₀ X₈₁ wherein X₆₂, X₆₅, X₆₆, X₆₈, X₆₉, X₇₁,
 X₇₃, X₇₆, X₇₇, X₇₈, X₈₀ and X₈₁ are any amino acid; X₆₃, X₇₀, and X₇₄ are
 hydrophobic amino acids; X₆₄ is a polar amino acid; X₆₇ and X₇₅ are
 aromatic amino acids; and X₇₂ and X₇₉ are cysteines.

214. The amino acid sequence according to claim 203 wherein at least one of the
 20 sequences comprises HX₈₂X₈₃X₈₄X₈₅X₈₆X₈₇X₈₈X₈₉X₉₀X₉₁X₉₂ herein X₈₂ is
 proline or alanine; X₈₃ is a small amino acid; X₈₄ is selected from the group
 consisting of leucine, serine and threonine; X₈₅ is a polar amino acid; X₈₆ is
 any amino acid; X₈₇ is an aliphatic amino acid; X₈₈, X₈₉, X₉₀ is any amino
 acid; and X₉₁ and X₉₂ are aliphatic amino acids or
 25 X₁₀₄X₁₀₅X₁₀₆X₁₀₇X₁₀₈X₁₀₉X₁₁₀X₁₁₁X₁₁₂X₁₁₃X₁₁₄ wherein at least one of the
 amino acids of X₁₀₆ through X₁₁₁ are tryptophan; wherein X₁₀₄ and X₁₁₄ are
 both small amino acids; wherein X₁₀₅ is any amino acid; and wherein at least
 one of X₁₀₄, X₁₀₅, X₁₀₆ and one of X₁₁₂ X₁₁₃ X₁₁₄ are cysteine residues.

215. The amino acid sequence according to claim 203 wherein the two amino acid sequences are connected by a peptide or non-peptide linker.
216. The amino acid sequence according to claim 215 wherein the linker is a peptide consisting of about 2 to about 16 amino acids.
- 5 217. The amino acid sequence according to claim 215 wherein the linker is a non-peptide.
218. The amino acid sequence according to claim 217 wherein the linker is dialdehyde.
219. The amino acid sequence according to claim 203 wherein the amino acid
10 sequence is selected from the group consisting of

DYKDDDDKFHENFYDWFVRQVSGSGGLDALDRLMRYGEERPSLA
AAGAP,

DYKDDDDKFHENFYDWFVRQVSGGSHLCVLEELFWGASLFGYCSG
AAAGAPVPYPDPLEPRAA,

15 DYKDDDDKFHENFYDWFVRQVSGGSGGSGGSHLCVLEELFWGASL
FGYCSGAAAGAPVPYPDPLEPRAA,

DYKDDDDKFHENFYDWFVRQVSGGSGGSGGSGGSHLCVLEELFWG
ASLFGYCSGAAAGAPVPYPDPLEPRAA,

20 AQPAMAFHENFYDWFVRQVSGGSFHENFYDWFVRQVSAAAGAPVP
YPDPLEPRAA,

AQPAMAFHENFYDWFVRQVSGGSFHENFYDWFVRQVSGGSFHENF
YDWFVRQVSAAAGAPVPYPDPLEPRAA,

AQPAMAFHENFYDWFVRQVSGGSGGSFHENFYDWFVRQVSAAAG
APVPYPDPLEPRAA,

5 AQPAMAFHENFYDWFVRQVSGGSGGSGGSFHENFYDWFVRQVSAA
AGAPVPYPDPLEPRAA and

AQPAMAFHENFYDWFVRQVSGGSGGSGGSGGSFHENFYDWFVRQV
SAAAGAPVPYPDPLEPRAA.

10 220. A nucleic acid sequence encoding amino acid sequence which binds to IR at
Site 1 and/or Site 2, with the proviso that the sequence is not insulin, IGF, or
fragments thereof.

15 221. The nucleic acid sequence according to claim 220 wherein the nucleic acid
sequence encodes for an amino acid sequence selected from the group
consisting of FYDWF, FYEWF, FHENFYDWF, FHENFYDWFVRQVSK,
DYKDVTFTSAVFHENFYDWFVRQVSKK, GRVDWLQRNANFYDWFV
AELG and APTFYAWFNQQT.

20 222. The nucleic acid sequence according to claim 220 wherein the nucleic acid
sequence encodes for an amino acid sequence selected from the group
consisting of DYKDFYDAIDQLVRGSARAGGTRDKK and
KDRAFYNGLRDLVGAVYGAWDKK.

223. The nucleic acid sequence according to claim 220 wherein the nucleic acid
sequence encodes for an amino acid sequence selected from the group
consisting of SFYEAIHQLLGV,

NSFYEALRMLSS,
SLNFYDALQLLA,
SSNFYQALMLLS,
SDGFYNAIELLS,
HETFYSMIRSLA,
HDPFYSMMKSL and
WSDFYSYFQGL.

- 5
224. A kit for identifying a compound which binds IGF-1 receptor, comprising a IGF-1 receptor and an amino acid sequence selected from Formulas 1-10, or
10 the amino acid sequences of Figures 9-11, which bind to the receptor at Site 1 or Site 2.
225. The kit according to claim 224, wherein the amino acid sequence comprises the amino acid sequence FYDWF.
226. The kit according to claim 225, wherein the amino acid sequence comprises
15 the amino acid sequence SAKNFYDWFVKK.
227. The kit according to claim 226 wherein the amino acid sequence comprises the amino acid sequence FYSLLASL.
228. The kit according to claim 227 wherein the amino acid sequence comprises the amino acid sequence QMKDIFYSLLASLAACK.
- 20 229. A kit for identifying a compound which binds IR comprising IR and an amino acid sequence selected from Formulas 1-10 or the amino acid sequences of Figures 9 and 11 which bind IR at Site 1 or Site 2.
230. A pharmaceutical composition comprising a amino acid sequence which binds specifically to IGF-1 receptor at Site 1 and is an IGF agonist, with the
25 proviso that the amino acid sequence is not IGF-1, insulin, or fragments thereof, and a pharmaceutically acceptable carrier.

231. The composition according to claim 230, wherein the peptide comprises the amino acid sequence NFYDWFV.
232. The pharmaceutical composition according to claim 230, wherein the peptide comprises the amino acid sequence QMKDIFYSLLASLAA.
- 5 233. A pharmaceutical composition comprising a amino acid sequence which binds specifically to IR receptor at Site 1 and is an insulin agonist, with the proviso that the amino acid sequence is not insulin, IGF, or fragments thereof, and a pharmaceutically acceptable carrier.
- 10 234. The pharmaceutical composition according to claim 233, wherein the peptide comprises the amino acid sequence FYDWF.
235. The pharmaceutical composition according to claim 233, wherein the peptide comprises the amino acid sequence FYSLLASL.
- 15 236. A method of treating diabetes comprising administering to an individual in need of treatment a therapeutically effective amount of an amino acid sequence which binds IR at Site 1 and is an insulin agonist, with the proviso that the amino acid sequence is not insulin, IGF, or fragments thereof.
237. The method according to claim 236 wherein the amino acid sequence is expressed by a recombinant vector administered to the individual.
- 20 238. The method according to claim 236 wherein the amino acid sequence is administered to the individual as a polypeptide.

239. A method of treating a patient with an IGF sensitive tumor comprising administering to an individual in need of treatment a therapeutically effective amount of an amino acid sequence which is an IGF-1R antagonist, with the proviso that the amino acid sequence is not insulin, IGF, or fragments thereof.
240. The method according to claim 239 wherein the amino acid sequence is expressed by a recombinant vector administered to the individual.
241. The method according to claim 239 wherein the amino acid sequence is administered to the individual as a polypeptide.
242. A method of screening for a compound which binds to IR comprising:
- i) immobilizing IR, or a fragment thereof, on a surface;
 - ii) incubating the IR, or fragment thereof, with a known amount of labeled amino acid sequence of Formulas 1-10, or an amino acid sequence selected from Figures 10-11, which binds IR and a compound to be screened under conditions which provide for binding of the labeled amino acid sequence to bind IR;
 - iii) measuring the amount of labeled amino acid sequence bound to IR;
 - iv) determining from the amount of bound labeled peptide whether the compound has competitively bound to IR.
243. An amino acid sequence capable of binding to Site 1 or Site 2 of IR identified by the method according to claim 242, with the proviso that the amino acid sequence is not insulin, IGF, or fragments thereof.
244. The amino acid sequence according to claim 243 wherein the amino acid sequence is an IR agonist.

245. The amino acid sequence according to claim 243 wherein the amino sequence binds to Site 1 of IR.
246. The amino acid sequence according to claim 243 wherein the amino sequence binds to Site 2 of IR.
- 5 247. A method of screening for a compound which binds to IGF-1R comprising:
- i) immobilizing IGF-1R, or a fragment thereof, on a surface;
 - ii) incubating the IGF-1R, or fragment thereof, with a known amount of labeled amino acid sequence of Formulas 1-9, or an amino acid sequence selected from Figure 10, which binds IGF-1R and a compound to be screened under
 - 10 conditions which provide for binding of the labeled amino acid sequence to bind to IGF-1R;
 - iii) measuring the amount of labeled amino acid sequence bound to IGF-1R;
 - iv) determining from the amount of bound labeled peptide
 - 15 whether the compound has competitively bound to IGF-1R.
248. An amino acid sequence capable of bind to Site 1 or Site 2 of IGF-1R identified by the method according to claim 247, with the proviso that the amino acid sequence is not insulin, IGF, or fragments thereof.
249. The amino acid sequence according to claim 248 wherein the amino acid
- 20 sequence is an IGF agonist.
250. The amino acid sequence according to claim 248 wherein the amino sequence binds to Site 1 of IGF-1R.

251. The amino acid sequence according to claim 248 wherein the amino sequence binds to Site 2 of IGF-1R.
252. An amino acid sequence comprising the sequence $WX_{123}GYX_{124}WX_{125}X_{126}$ wherein X_{123} is proline, glycine, serine, arginine, alanine or leucine, X_{124} is any amino acid; X_{125} is a hydrophobic amino acid; and X_{126} is any amino acid.
253. The amino acid sequence according to claim 252 wherein X_{123} is proline and X_{125} is leucine or phenylalanine.
254. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 1.
255. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 2.
256. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 3.
257. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 4.
258. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 5.
259. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 6.

- 260. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 7.
- 261. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 8.
- 5 262. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 9.
- 263. A recombinant peptide library comprising members wherein the majority of the members comprise an amino acid sequence of Formula 10.